

SEQUENCE LISTING

<110> ERIKSSON, Ulf
AASE, Karin
LI, Xuri
PONTEN, Annica
UUTELA, Marko
ALITALO, Kari
OESTMAN, Arne
HELDIN, Carl-Henrik

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Thr Val Glu Asp Leu Leu Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu

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Asp Leu Glu Asn Met Tyr Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser
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Tyr His Asp Arg Lys Ser Lys Val Asp Leu Asp Arg Leu Asn Asp Asp
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Ala Lys Arg Tyr Ser Cys Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg
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Glu Glu Leu Lys Leu Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu
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Ser Cys Thr Cys Asn Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val
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| cag | agt | cct | aga | ttc | ccg | aac | agc | tac | ccc | agg | aac | ctg | ctc | ctg | aca | 96 | |
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| | | 35 | | | | | 40 | | | | | 45 | | | | | |
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| | | | | | | | | | | | | | | | | | |
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| Phe | Val | Glu | Val | Glu | Asp | Ile | Ser | Glu | Thr | Ser | Thr | Ile | Ile | Arg | Gly | | |
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| | | | | | | | | | | | | | | | | | |
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| Arg | Trp | Cys | Gly | His | Lys | Glu | Val | Pro | Pro | Arg | Ile | Lys | Ser | Arg | Thr | | |
| | | | | 85 | | | | 90 | | | | | | 95 | | | |
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| aac | caa | att | aaa | atc | aca | ttc | aag | tcc | gat | gac | tac | ttt | gtg | gct | aaa | 336 | |
| Asn | Gln | Ile | Lys | Ile | Thr | Phe | Lys | Ser | Asp | Asp | Tyr | Phe | Val | Ala | Lys | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
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| Pro | Gly | Phe | Lys | Ile | Tyr | Tyr | Ser | Leu | Leu | Glu | Asp | Phe | Gln | Pro | Ala | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| | | | | | | | | | | | | | | | | | |
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| Ala | Leu | Asp | Lys | Lys | Ile | Ala | Glu | Phe | Asp | Thr | Val | Glu | Asp | Leu | Leu | | |
| | | | 165 | | | | | 170 | | | | | | 175 | | | |
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| aag | tac | ttc | aat | cca | gag | tca | tgg | caa | gaa | gat | ctt | gag | aat | atg | tat | 576 | |
| Lys | Tyr | Phe | Asn | Pro | Glu | Ser | Trp | Gln | Glu | Asp | Leu | Glu | Asn | Met | Tyr | | |
| | | | 180 | | | | 185 | | | | | | 190 | | | | |
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| ctg | gac | acc | cct | cgg | tat | cga | ggc | agg | tca | tac | cat | gac | cgg | aag | tca | 624 | |
| Leu | Asp | Thr | Pro | Arg | Tyr | Arg | Gly | Arg | Ser | Tyr | His | Asp | Arg | Lys | Ser | | |
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| Thr | Pro | Arg | Asn | Tyr | Ser | Val | Asn | Ile | Arg | Glu | Glu | Leu | Lys | Leu | Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Asn | Val | Val | Phe | Phe | Pro | Arg | Cys | Leu | Leu | Val | Gln | Arg | Cys | Gly | Gly | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Asn | Cys | Gly | Cys | Gly | Thr | Val | Asn | Trp | Arg | Ser | Cys | Thr | Cys | Asn | Ser | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | 260 | | | | | | | | | | | 265 | | | | | | | | | | | 270 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Gly | Lys | Thr | Val | Lys | Lys | Tyr | His | Glu | Val | Leu | Gln | Phe | Glu | Pro | Gly | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| His | Ile | Lys | Arg | Arg | Gly | Arg | Ala | Lys | Thr | Met | Ala | Leu | Val | Asp | Ile | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | 290 | | | | | | | | | | | 295 | | | | | | | | | | | 300 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Gln | Leu | Asp | His | His | Glu | Arg | Cys | Asp | Cys | Ile | Cys | Ser | Ser | Arg | Pro | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 305 | | | | | | | | | | | 310 | | | | | | | | | | | 315 | | | | | | | | | | | 320 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| acccctccac | | | | | | | | | | | | | | | | aaaagcaaat | | | | | | | | | | | | | | | | cctttcaaga | | | | | | | | | | | | | | | | atggcatggg | | | | | | | | | | | | | | | | cattctgtat | | | | | | | | | | | | | | | | gaacctttcc | | | | | | | | | | | | | | | | 1856 |

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20 25 30

Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
35 40 45

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
50 55 60

Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
65 70 75 80

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
85 90 95

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
100 105 110

Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
115 120 125

Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
130 135 140

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
145 150 155 160

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Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
165 170 175

Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
180 185 190

Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
195 200 205

Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
210 215 220

Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
225 230 235 240

Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
245 250 255

Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
260 265 270

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
275 280 285

His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
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Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
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| ggagcagaac ccggcttttt cttggagcga cgctgtctct agtcgctgat cccaa atg | 178 |
| | Met |
| | 1 |
| cac cgg ctc atc ttt gtc tac act cta atc tgc gca aac ttt tgc agc | 226 |
| His Arg Leu Ile Phe Val Tyr Thr Leu Ile Cys Ala Asn Phe Cys Ser | |
| | 5 10 15 |
| tgt cgg gac act tct gca acc ccg cag agc gca tcc atc aaa gct ttg | 274 |
| Cys Arg Asp Thr Ser Ala Thr Pro Gln Ser Ala Ser Ile Lys Ala Leu | |
| | 20 25 30 |
| cgc aac gcc aac ctc agg cga gat gag agc aat cac ctc aca gac ttg | 322 |
| Arg Asn Ala Asn Leu Arg Arg Asp Glu Ser Asn His Leu Thr Asp Leu | |
| | 35 40 45 |
| tac cga aga gat gag acc atc cag gtg aaa gga aac ggc tac gtg cag | 370 |
| Tyr Arg Arg Asp Glu Thr Ile Gln Val Lys Gly Asn Gly Tyr Val Gln | |
| | 50 55 60 65 |
| agt cct aga ttc ccg aac agc tac ccc agg aac ctg ctc ctg aca tgg | 418 |
| Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp | |
| | 70 75 80 |
| cgg ctt cac tct cag gag aat aca cgg ata cag cta gtg ttt gac aat | 466 |
| Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp Asn | |
| | 85 90 95 |
| cag ttt gga tta gag gaa gca gaa aat gat atc tgt agg tat gat ttt | 514 |
| Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe | |
| | 100 105 110 |
| gtg gaa gtt gaa gat ata tcc gaa acc agt acc att att aga gga cga | 562 |
| Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly Arg | |
| | 115 120 125 |
| tgg tgt gga cac aag gaa gtt cct cca agg ata aaa tca aga acg aac | 610 |
| Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr Asn | |
| | 130 135 140 145 |
| caa att aaa atc aca ttc aag tcc gat gac tac ttt gtg gct aaa cct | 658 |
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55

60

Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr
65 70 75 80

Trp Arg Leu His Ser Gln Glu Asn Thr Arg Ile Gln Leu Val Phe Asp
85 90 95

Asn Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp
100 105 110

Phe Val Glu Val Glu Asp Ile Ser Glu Thr Ser Thr Ile Ile Arg Gly
115 120 125

Arg Trp Cys Gly His Lys Glu Val Pro Pro Arg Ile Lys Ser Arg Thr
130 135 140

Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys
145 150 155 160

Pro Gly Phe Lys Ile Tyr Tyr Ser Leu Leu Glu Asp Phe Gln Pro Ala
165 170 175

Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Ile Ser Gly
180 185 190

Val Ser Tyr Asn Ser Pro Ser Val Thr Asp Pro Thr Leu Ile Ala Asp
195 200 205

Ala Leu Asp Lys Lys Ile Ala Glu Phe Asp Thr Val Glu Asp Leu Leu
210 215 220

Lys Tyr Phe Asn Pro Glu Ser Trp Gln Glu Asp Leu Glu Asn Met Tyr
225 230 235 240

Leu Asp Thr Pro Arg Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser
245 250 255

Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Ala Lys Arg Tyr Ser Cys
260 265 270

Thr Pro Arg Asn Tyr Ser Val Asn Ile Arg Glu Glu Leu Lys Leu Ala
275 280 285

Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
290 295 300

Asn Cys Gly Cys Gly Thr Val Asn Trp Arg Ser Cys Thr Cys Asn Ser
305 310 315 320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro Gly
325 330 335

His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp Ile
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Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
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Pro Arg
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<400> 9

Arg Lys Ser Lys
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<211> 91

<212> PRT

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<213> Homo sapiens

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<221> misc_feature

<223> PDGF/VEGF-homology domain of PDGF-D

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Ala Asn Val Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly
20 25 30

Gly Asn Cys Gly Cys Gly Thr Val Lys Leu Glu Ser Cys Thr Cys Asn
35 40 45

Ser Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Gln Phe Glu Pro
50 55 60

Gly His Ile Lys Arg Arg Gly Arg Ala Lys Thr Met Ala Leu Val Asp
65 70 75 80

Ile Gln Leu Asp His His Glu Arg Cys Asp Cys
85 90

<210> 11

<211> 88

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<213> Homo sapiens

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<223> PDGF/VEGF-homology domain of PDGF-C

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Arg Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg
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Lys Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu
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Glu Cys Ala Cys

<210> 13

<211> 84

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<223> PDGF/VEGF-homology domain of PDGF-B

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20 25 30

Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
35 40 45

Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
50 55 60

Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
65 70 75 80

Ala Cys Lys Cys

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35 40 45
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50 55 60
Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys Glu Cys
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<210> 16

<211> 78

<212> PRT

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<223> PDGF/VEGF-homology domain of VEGF-B167

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20 25 30
Gly Gly Cys Cys Pro Asp Asp Gly Leu Glu Cys Val Pro Thr Gly Gln
35 40 45
His Gln Val Arg Met Gln Ile Leu Met Ile Arg Tyr Pro Ser Ser Gln

60

Leu Gly Glu Met Ser Leu Glu Glu His Ser Gln Cys Glu Cys
65 70 75

<213> Homo sapiens

<223> PDGF/VEGF-homology domain of VEGF-C

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Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
20 25 30

Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
35 40 45

Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
50 55 60

Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg
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Cys

<212> PRT

2049060" e229900f

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<223> PDGF/VEGF-homology domain of VEGF-D

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20 25 30

Gly Gly Cys Cys Asn Glu Glu Gly Val Met Cys Met Asn Thr Ser Thr
35 40 45

Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser
50 55 60

Val Pro Glu Leu Val Pro Val Lys Ile Ala Asn His Thr Gly Cys Lys
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Cys

<210> 19

<211> 118

<212> PRT

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35 40 45

Tyr Arg Ser Arg Leu Cys Trp Tyr Asp Tyr Val Glu Val Arg Asp Gly
50 55 60

Phe Trp Arg Lys Ala Pro Leu Arg Gly Arg Phe Cys Gly Ser Lys Leu
65 70 75 80

Pro Glu Pro Ile Val Ser Thr Asp Ser Arg Leu Trp Val Glu Phe Arg
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Ser Ser Ser Asn Trp Val Gly Lys Gly Phe Phe Ala Val Tyr Glu Ala
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<223> CUB domain 2 of BMP-1

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20 25 30

Val Ser Glu Gly Phe His Val Gly Leu Thr Phe Gln Ser Phe Glu Ile

35

40

45

Glu Arg Met Asp Ser Cys Ala Tyr Asp Tyr Leu Glu Val Arg Asp Gly
50 55 60

His Ser Glu Ser Ser Thr Leu Ile Gly Arg Tyr Cys Gly Tyr Glu Lys
65 70 75 80

Pro Asp Asp Ile Lys Ser Thr Ser Ser Arg Leu Trp Leu Lys Phe Val
85 90 95

Ser Asp Gly Ser Ile Asn Lys Ala Gly Phe Ala Val Asn Phe Phe Lys
100 105 110

<210> 22

<211> 113

<212> PRT

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20 25 30

Ala Pro Thr Gln Tyr Arg Ile Ser Leu Gln Phe Asp Phe Phe Glu Thr
35 40 45

Glu Gly Asn Asp Val Cys Lys Tyr Asp Phe Val Glu Val Arg Ser Gly
50 55 60

Leu Thr Ala Asp Ser Lys Leu His Gly Lys Phe Cys Gly Ser Glu Lys
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Val Ser Asp Tyr Glu Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu
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<210> 24

<211> 119

<212> PRT

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Phe Pro Glu Lys Tyr Pro Asn Ser Leu Glu Cys Thr Tyr Ile Val Phe
20 25 30

Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe Asp Leu
35 40 45

Glu Pro Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr Asp Arg
50 55 60

Leu Glu Ile Trp Asp Gly Phe Pro Asp Val Gly Pro His Ile Gly Arg
65 70 75 80

Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser Gly Ile
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Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu Gly Phe
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Ser Ala Asn Tyr Ser Val Leu
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<223> can be any amino acid residue

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<210> 26

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Forward PCR primer used to amplify a 327 bp DNA fragment from a human fetal lung cDNA library

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<211> 20

<212> DNA

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<210> 28

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<223> Description of Artificial Sequence: Adaptor primer 1 (Clontech) used to amplify the sequence found at the 5' end of PDGF-D

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<210> 29

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Adaptor primer 2 (Clontech) used to amplify the sequence found at the 5' end of PDGF-D

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<213> Artificial Sequence

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<210> 31
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<210> 32
<211> 345
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Amino acid sequence for PDGF-C

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Met Ser Leu Phe Gly Leu Leu Leu Val Thr Ser Ala Leu Ala Gly Gln
1 5 10 15

Arg Arg Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
20 25 30

Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
35 40 45

Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
50 55 60

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Thr | Tyr | Pro | Arg | Asn | Thr | Val | Leu | Val | Trp | Arg | Leu | Val | Ala | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
85 90 95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
100 105 110

Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
115 120 125

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Gly | Lys | Gln | Ile | Ser | Lys | Gly | Asn | Gln | Ile | Arg | Ile | Arg | Phe |
| | 130 | | | | | 135 | | | | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Asp | Glu | Tyr | Phe | Pro | Ser | Glu | Pro | Gly | Phe | Cys | Ile | His | Tyr |
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Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
165 170 175

Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
180 185 190

Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
195 200 205

Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
210 215 220

Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225 230 235 240

Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
245 250 255

Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
260 265 270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
275 280 285

His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lys Lys
290 295 300

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Arg Gly Leu
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His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
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<223> Primer includes a XbaI site for in frame cloning

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gatgagagca atcacctcac agacttgtac cagagagagg agaacattca ggtgacaagc 180
aatggccatg tgcagagtcc tcgcttcccg aacagctacc caaggaacct gcttctgaca 240
tggtggctcc gttcccagga gaaaacacgg atacaactgt cctttgacca tcaattcgga 300
ctagaggaag cagaaaatga cattttagg tatgactttg tggaagttga agaagtctca 360

| | | | | |
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| 50 | | 55 | | 60 |
| Gln Ser Pro Arg Phe Pro Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr | 65 | 70 | 75 | 80 |
| Trp Trp Leu Arg Ser Gln Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp | 85 | 90 | 95 | |
| His Gln Phe Gly Leu Glu Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp | 100 | 105 | 110 | |
| Phe Val Glu Val Glu Glu Val Ser Glu Ser Ser Thr Val Val Arg Gly | 115 | 120 | 125 | |
| Arg Trp Cys Gly His Lys Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr | 130 | 135 | 140 | |
| Asn Gln Ile Lys Ile Thr Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys | 145 | 150 | 155 | 160 |
| Pro Gly Phe Lys Ile Tyr Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu | 165 | 170 | 175 | |
| Ala Ala Ser Glu Thr Asn Trp Glu Ser Val Thr Ser Ser Phe Ser Gly | 180 | 185 | 190 | |
| Val Ser Tyr His Ser Pro Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp | 195 | 200 | 205 | |
| Ala Leu Asp Lys Thr Val Ala Glu Phe Asp Thr Val Glu Asp Leu Leu | 210 | 215 | 220 | |
| Lys His Phe Asn Pro Val Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr | 225 | 230 | 235 | 240 |
| Leu Asp Thr Pro His Tyr Arg Gly Arg Ser Tyr His Asp Arg Lys Ser | 245 | 250 | 255 | |
| Lys Val Asp Leu Asp Arg Leu Asn Asp Asp Val Lys Arg Tyr Ser Cys | 260 | 265 | 270 | |
| Thr Pro Arg Asn His Ser Val Asn Leu Arg Glu Glu Leu Lys Leu Thr | 275 | 280 | 285 | |

Asn Ala Val Phe Phe Pro Arg Cys Leu Leu Val Gln Arg Cys Gly Gly
290 295 300

Asn Cys Gly Cys Gly Thr Val Asn Trp Lys Ser Cys Thr Cys Ser Ser
305 310 315 320

Gly Lys Thr Val Lys Lys Tyr His Glu Val Leu Lys Phe Glu Pro Gly
325 330 335

His Phe Lys Arg Arg Gly Lys Ala Lys Asn Met Ala Leu Val Asp Ile
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Gln Leu Asp His His Glu Arg Cys Asp Cys Ile Cys Ser Ser Arg Pro
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| gatgacttgt accagagaga ggagaacatt caggtgacaa gcaatggcca tgtgcagagt | 180 |
| cctcgcttcc cgaacagcta cccaaggaac ctgcttctga catggtggct ccgttcccag | 240 |
| gagaaaacac ggatacaact gtcctttgac catcaattcg gactagagga agcagaaaat | 300 |
| gacatttgta ggtatgactt tgtggaagtt gaagaagtct cagagagcag cactgttgtc | 360 |
| agaggaagat ggtgtggcca caaggagatc cctccaagga taacgtcaag aacaaaccag | 420 |
| attaaaaatca catttaagtc tgatgactac tttgtggcaa aacctggatt caagatttat | 480 |
| tattcatttg tggaagattt ccaaccggaa gcagcctcag agaccaactg ggaatcagtc | 540 |
| acaagctctt tctctggggt gtcctatcac tctccatcaa taacggaccc cactctcact | 600 |

gctgatgccc tggacaaaac tgtcgcagaa ttcgataccg tggagatct acttaagcac 660
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Cys Tyr Pro Asp Thr Phe Ala Thr Pro Gln Arg Ala Ser Ile Lys Ala
 20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Asp Leu Tyr Gln Arg Glu Glu
 35 40 45

Asn Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro
 50 55 60

Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln
 65 70 75 80

Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu
 85 90 95

2046602299001

Tyr His Glu Val Leu Lys Phe Glu Pro Gly His Phe Lys Arg Arg Gly
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Lys Ala Lys Asn Met Ala Leu Val Asp Ile Gln Leu Asp His His Glu
340 345 350

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gatgacttgt accagagaga ggagaacatt caggtgacaa gcaatggcca tgtgcagagt 180
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gacatttgta ggtatgactt tgtggaagtt gaagaagtct cagagagcag cactgttgtc 360
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20 25 30

Leu Arg Asn Ala Asn Leu Arg Arg Asp Asp Leu Tyr Gln Arg Glu Glu
35 40 45

Asn Ile Gln Val Thr Ser Asn Gly His Val Gln Ser Pro Arg Phe Pro
50 55 60

Asn Ser Tyr Pro Arg Asn Leu Leu Leu Thr Trp Trp Leu Arg Ser Gln
65 70 75 80

Glu Lys Thr Arg Ile Gln Leu Ser Phe Asp His Gln Phe Gly Leu Glu
85 90 95

Glu Ala Glu Asn Asp Ile Cys Arg Tyr Asp Phe Val Glu Val Glu Glu
100 105 110

Val Ser Glu Ser Ser Thr Val Val Arg Gly Arg Trp Cys Gly His Lys
115 120 125

Glu Ile Pro Pro Arg Ile Thr Ser Arg Thr Asn Gln Ile Lys Ile Thr
130 135 140

Phe Lys Ser Asp Asp Tyr Phe Val Ala Lys Pro Gly Phe Lys Ile Tyr
145 150 155 160

Tyr Ser Phe Val Glu Asp Phe Gln Pro Glu Ala Ala Ser Glu Thr Asn
165 170 175

Trp Glu Ser Val Thr Ser Ser Phe Ser Gly Val Ser Tyr His Ser Pro
180 185 190

Ser Ile Thr Asp Pro Thr Leu Thr Ala Asp Ala Leu Asp Lys Thr Val
195 200 205

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Ala Glu Phe Asp Thr Val Glu Asp Leu Leu Lys His Phe Asn Pro Val
210 215 220

Ser Trp Gln Asp Asp Leu Glu Asn Leu Tyr Leu Asp Thr Pro His Tyr
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